

FIGURE 1

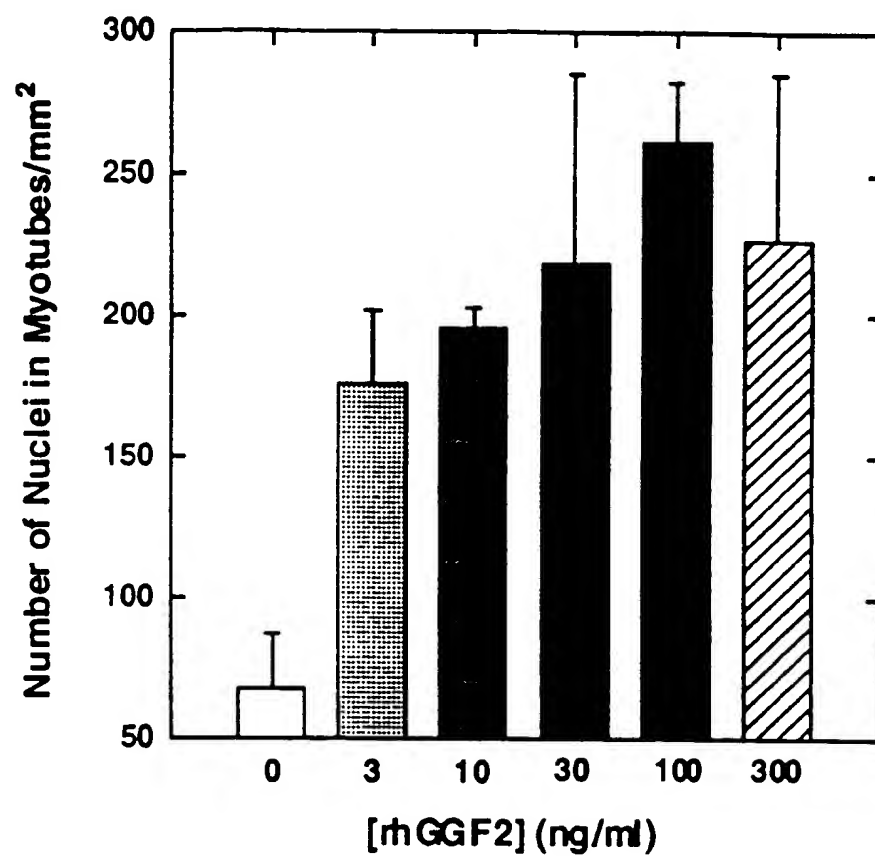


FIGURE 2

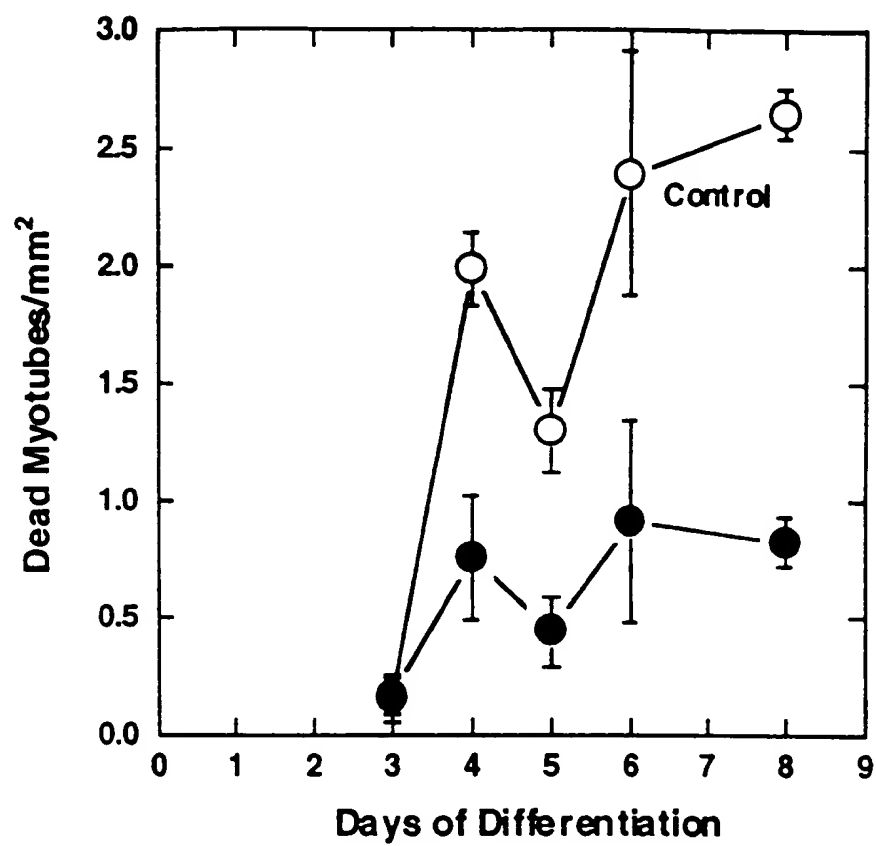


FIGURE 3

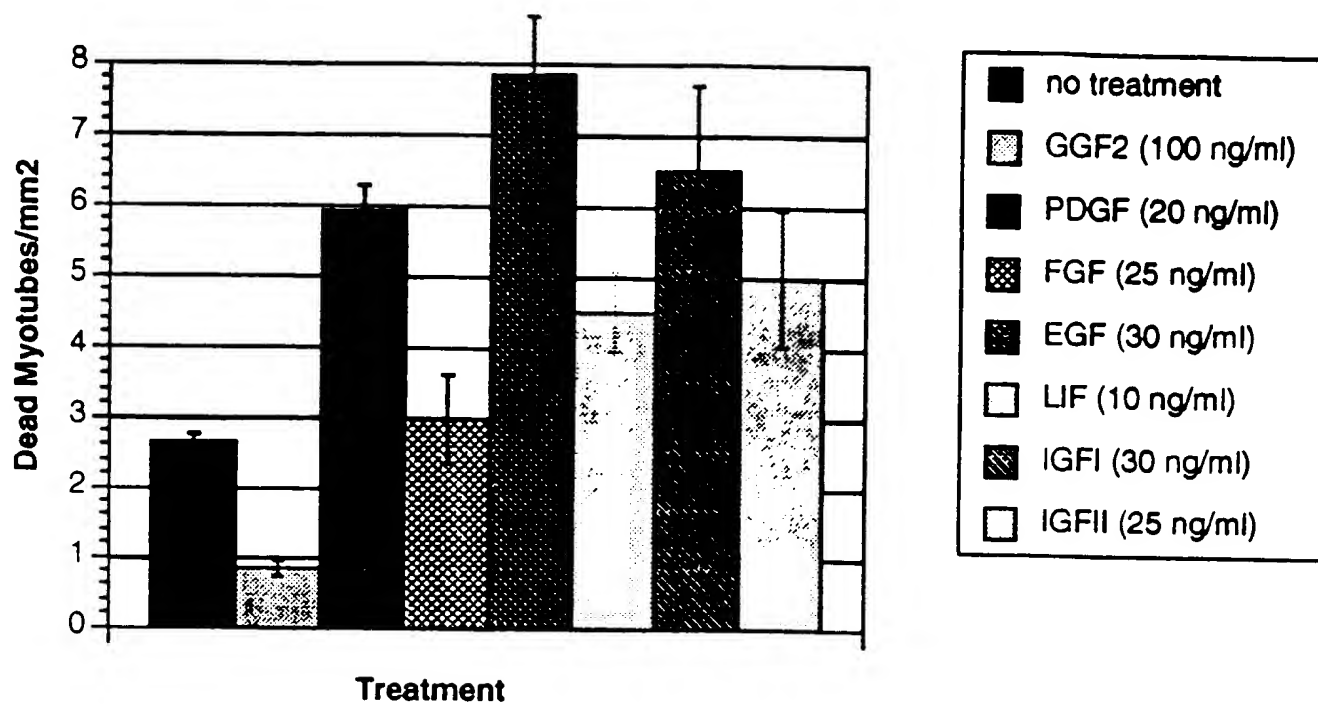


FIGURE 4

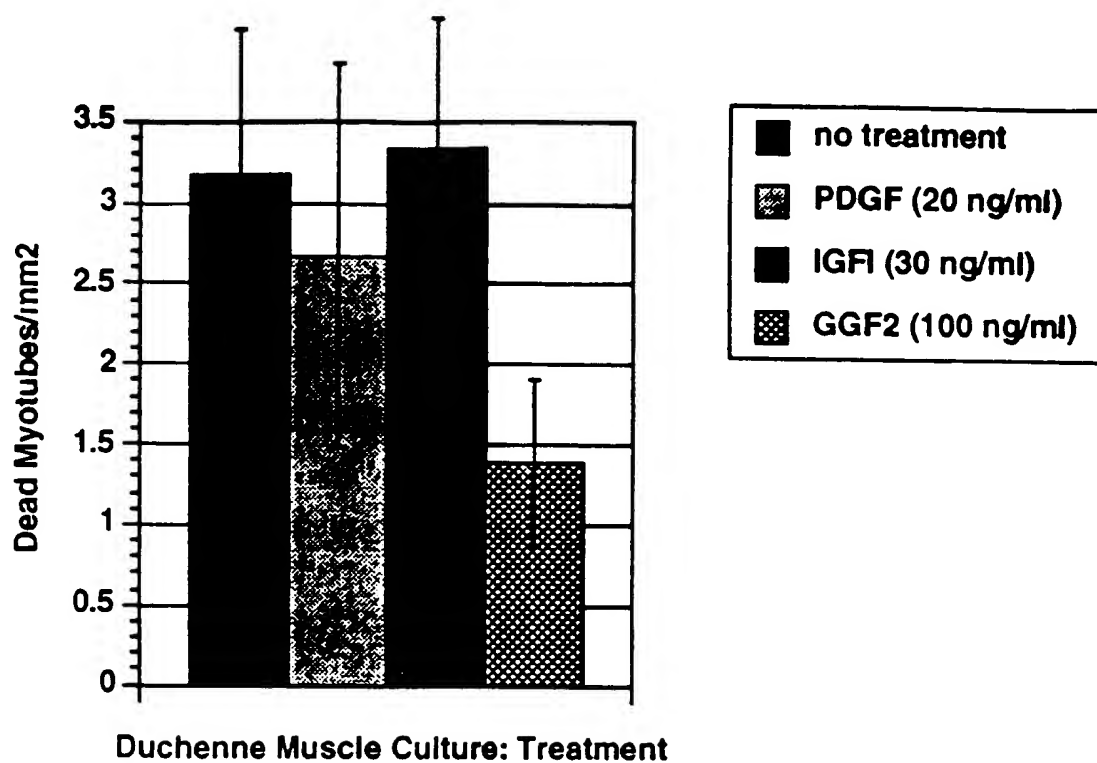


FIGURE 5

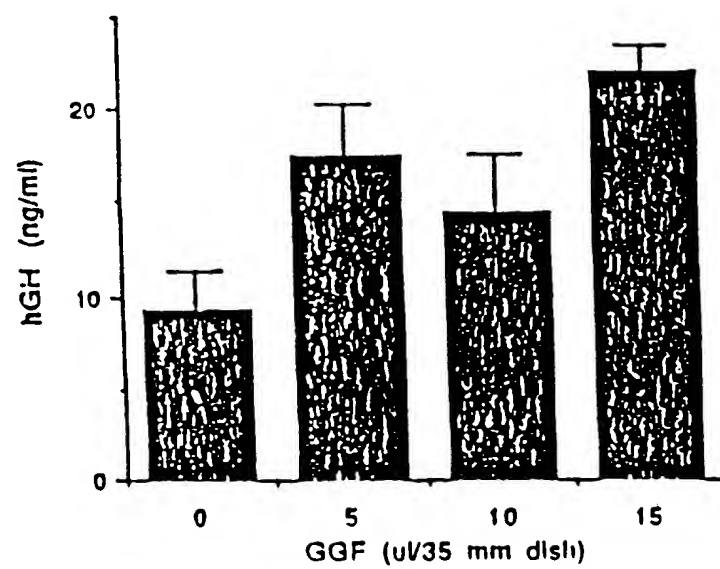


FIGURE 6

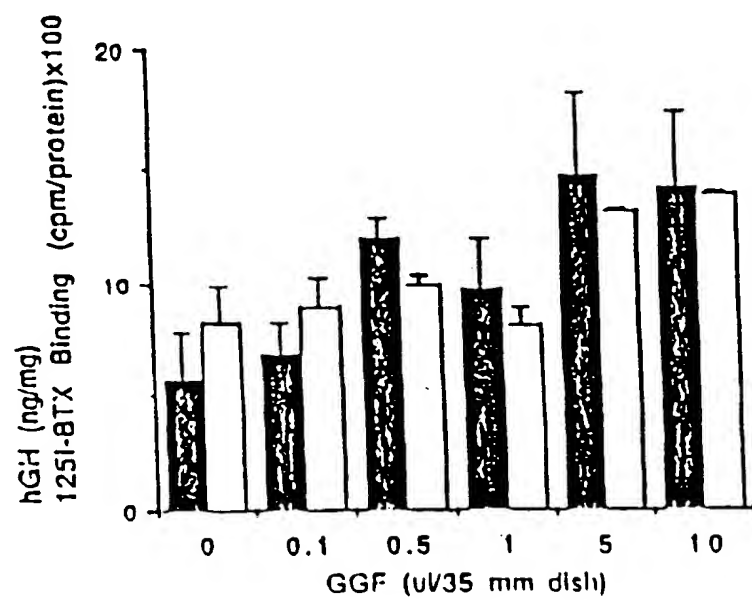


FIGURE 7

FIGURE 8

1F-1 01	Membrane	F K G D A M T E (seq 18 no: 1)	
1F-1 02	Trypsin peptides	K R A S L A D E Y E Y M X K . (seq 18 no: 2)	
1F-1 03		K R T E T S S G L X L K . (seq 18 no: 3)	
1F-1 04		K R K L G E M W A E (seq 18 no: 4)	
1F-1 05		K R L G E K R A (seq 18 no: 5)	
1F-1 06		K R I K S E H A G L S I G D T A K . (seq 18 no: 6)	18AG-1
1F-1 07		K R A S M A D E Y E Y M R K . (seq 18 no: 7)	18AG-17
1F-1 08		K R I K G E H P G L S I G D V A K . (seq 18 no: 8)	18AG-2
1F-1 09		K R M S E Y A F F V Q T X R . (seq 18 no: 9)	18AG-1
1F-1 10		K R S E H P G L S I G D T A K . (seq 18 no: 10)	18AG-2
1F-1 11		K R A G V F A E X A R . (seq 18 no: 11)	18AG-1
1F-1 12		K R K L E F L X A K . (seq 18 no: 12)	
1F-1 13		K R T T E M A S E Q G A (seq 18 no: 13)	
1F-1 14		K R A K E A L A L K . (seq 18 no: 14)	
1F-1 15		K R F V L Q A K K . (seq 18 no: 15)	
1F-1 16		K R L G E M W (seq 18 no: 16)	18AG-1
1F-1 17	Proteome V8 peptides	E T O P D P G Q I L K K V P M V I G A Y T (seq 18 no: 169)	
1F-1 18		E Y K C L K F K W F K K A T V M (seq 18 no: 17)	
1F-1 19		E A K V F S K X D A (seq 18 no: 18)	
1F-1 20		E X K F Y V P (seq 18 no: 19)	18AG-1
1F-1 21		E L S F A S V R L P G C P P G V O P M V S F P V A L	18AG-1 (seq 18 no: 21)

FIGURE 9

A	OGF-1 01	FKGDANTE	(SEQ ID NO: 1)
	OGF-1 02	ASLADEYEYMXK	(SEQ ID NO: 22)
	OGF-1 03	TETSSGLXLK	(SEQ ID NO: 23)
	OGF-1 07	ASLADEYEYMRK	(SEQ ID NO: 24)
	OGF-1 11	AGYFAEXAR	(SEQ ID NO: 25)
	OGF-1 13	TTEMASEOGA	(SEQ ID NO: 26)
	OGF-1 14	AKZALALK	(SEQ ID NO: 27)
	OGF-1 15	FVLOAKK	(SEQ ID NO: 28)
	OGF-1 17	ETOPDPGOILKKVPHVIGAYT	(SEQ ID NO: 29)
	OGF-1 18	EYKCLKPKWPKATVM	(SEQ ID NO: 17)
B	OGF-1 20	EKKFYVP	(SEQ ID NO: 19)
	OGF-1 12	KLEPLXAK	(SEQ ID NO: 32)

KR VHQVWAAK.
KR YIFFMEPEAXSSG
KR LGAWGPPAFPVXY
KR WFVVEGK.
KR ALAAAGYDVEK.
KR LVLK.
KR XXYPGQITSN
KR ASPVSVGSVQELVQR.
KR VCLLTVAALPPT
KR D L L L X Y

GGF-II 01
GGF-II 02
GGF-II 03
GGF-II 04
GGF-II 05
GGF-II 06
GGF-II 07
GGF-II 08
GGF-II 09
GGF-II 10

(S2Q ID NO: 45)
(S2Q ID NO: 46)
(S2Q ID NO: 47)
(S2Q ID NO: 48)
(S2Q ID NO: 164)
(S2Q ID NO: 165)
(S2Q ID NO: 166)
(S2Q ID NO: 49)
(S2Q ID NO: 50)
(S2Q ID NO: 53)

Histone H1

Trypsin

KVHQVWAAK.
KASLADSGEYMXK.

GF-II 11
GF-II 12

(SEQ ID NO: 51)
(SEQ ID NO: 52)

FIGURE 11

A

GGF-II 01	VHQVWAAK	(SEQ ID NO: 45)
GGF-II 02	YIFFMEPEAXSSG	(SEQ ID NO: 46)
GGF-II 03	LGAWGPPAFPVXY	(SEQ ID NO: 47)
GGF-II 04	WFVVIEGK	(SEQ ID NO: 48)
GGF-II 06	ASPVSVGSVQELVQR	(SEQ ID NO: 49)
GGF-II 09	VCLLTVAALPPT	(SEQ ID NO: 50)
GGF-II 11	KVHQVWAAK	(SEQ ID NO: 51)
GGF-II 12	KASLADSGEYMXK	(SEQ ID NO: 52)

B

Novel Factor II Peptides - others

GGF-II 10	DLLLXY	(SEQ ID NO: 53)
-----------	--------	-----------------

Comparison of BrUdR JSA and ^{125}I UdR autoradiography method for the DNA synthesis assay in Schwann cell cultures

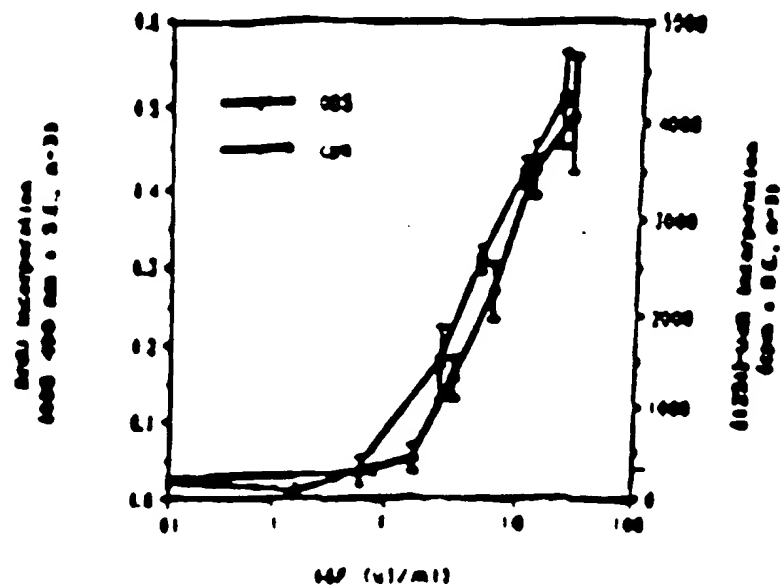


FIGURE 12

Comparison of Br-UdR immunoreactivity and Br-UdR labelled cell number

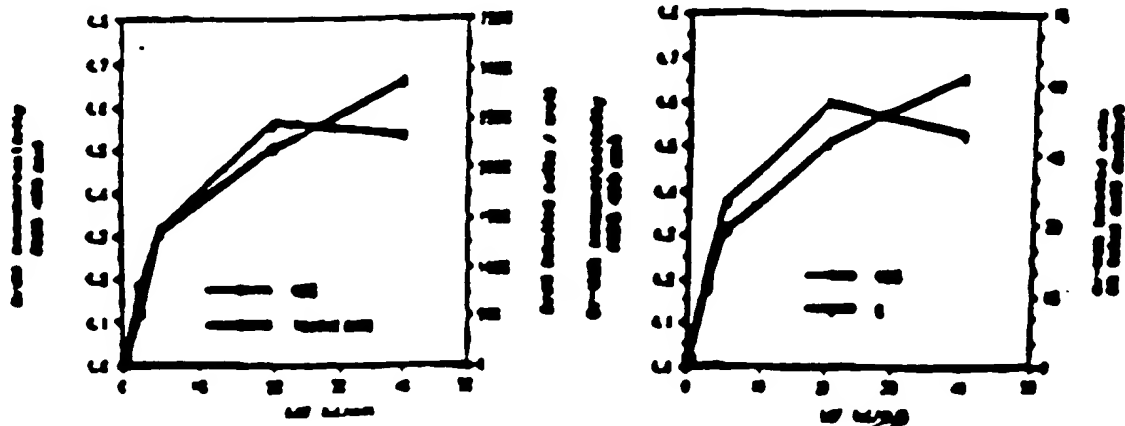


FIGURE 13A

FIGURE 13B

Mitogenic response of rat sciatic nerve Schwann cell to GGF₃

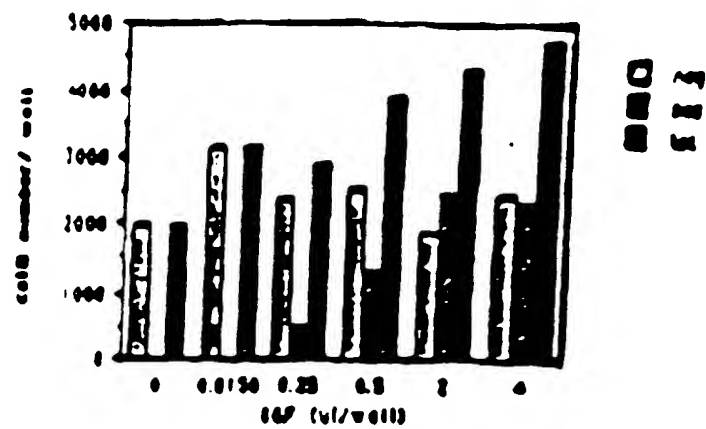


FIGURE 14

DNA synthesis in rat sciatic nerve Schwann cells and 3T3 fibroblasts in the presence of GGF₃

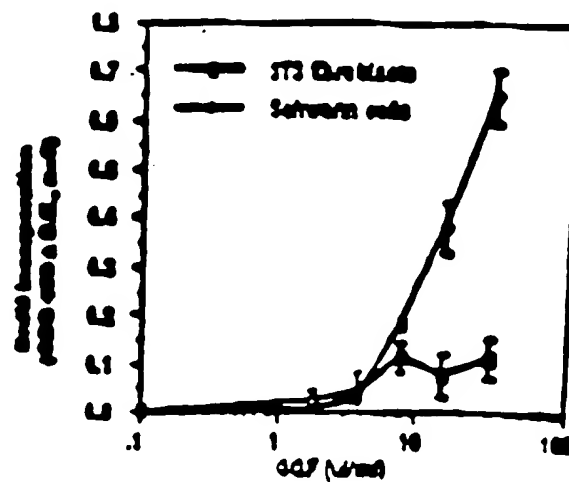


FIGURE 15

● Mitogenic response of BHK21 C13 cells
to FCS and GGFs

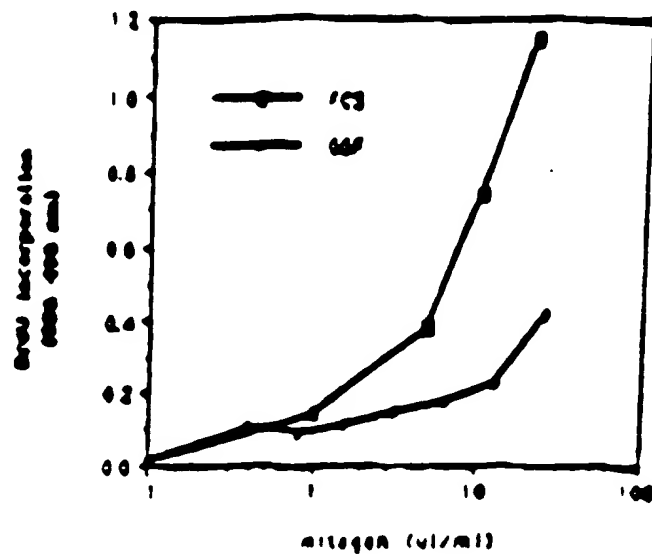


FIGURE 16

Survival and proliferation of BHK21 C13 cell
microcultures after 48 hours in presence of GGFs

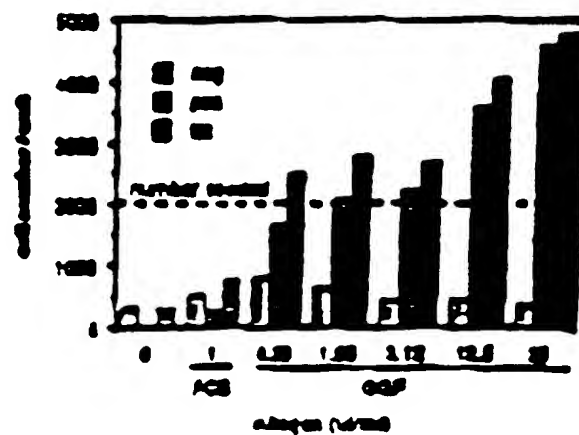


FIGURE 17

Mitogenic response of C6 cells to FCS

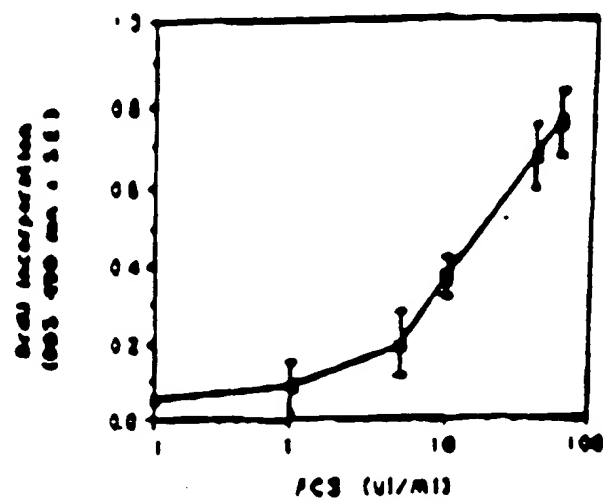


FIGURE 18

Mitogenic response of C6 cells to aFGF and GGFs

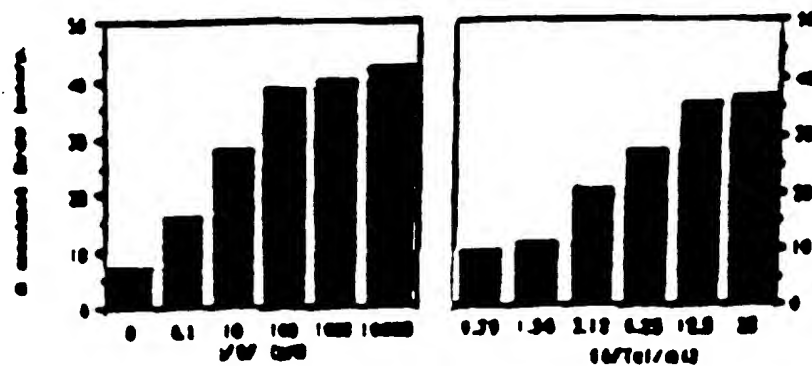


FIGURE 19

DEGENERATE OLIGONUCLEOTIDE PROBES FOR FACTOR I AND FACTOR II

Oligo	Sequence	Peptide	
535	TTYAAGGNGAYGCNCAYAC!	GGPI-1	(SEQ ID NO: 54)
536	CATRTAYTCRTAYTCRTONGC!	GGPI-2	(SEQ ID NO: 55)
537	TGYTCNGANGCCATYTCNGT!	GGPI-13	(SEQ ID NO: 56)
538	TGYTCNGTNGCCATYTCNGT!	GGPI-13	(SEQ ID NO: 57)
539	CCDATNACCATNGGNACTT!	GGPI-17	(SEQ ID NO: 58)
540	GCHGCCCAUACYTGTGAC!	GGPII-1	(SEQ ID NO: 59)
541	GCYTCNGGYTCATRAAAA!	GGPII-2	(SEQ ID NO: 60)
542	CCYTCDATNACUACUACCA!	GGPII-4	(SEQ ID NO: 61)
543	TCHGCCAARTANGCCG!	GGPI-11	(SEQ ID NO: 62)
544	GCHGCHAGNGCTTCYTTNGC!	GGPI-14	(SEQ ID NO: 63)
545	GCHGCCYANGCTTCYTTNGC!	GGPI-14	(SEQ ID NO: 64)
546	TTYTTNGCYTGNAGAACAA!	GGPI-15	(SEQ ID NO: 65)
551	TTYTTNGCYTGYAUAACAA!	GGPI-15	(SEQ ID NO: 66)
558	TGNACUAGYTCYTGAC!	GGPII-6	(SEQ ID NO: 67)
559	TGNACYAAATCYTGAC!	GGPII-6	(SEQ ID NO: 68)
609	CATRTAYTCCHGARTONGC!	GGPII-12	(SEQ ID NO: 69)
610	CATRTAYTCCHGCTRTONGC!	GGPII-12	(SEQ ID NO: 70)
649	NGARTCHGCYANGANGCYTT!	GGPII-12	(SEQ ID NO: 71)
650	NGARTCHGCUANGANGCYTT!	GGPII-12	(SEQ ID NO: 72)
651	RCTRTCHGCYANGANGCYTT!	GGPII-12	(SEQ ID NO: 73)
652	RCTRTCHGCUANGANGCYTT!	GGPII-12	(SEQ ID NO: 74)
653	NGARTCHGCYAACTNGCYTT!	GGPII-12	(SEQ ID NO: 75)
654	NGARTCHGCNAGCTNGCYTT!	GGPII-12	(SEQ ID NO: 76)
655	RCTRTCHGCYAACTNGCYTT!	GGPII-12	(SEQ ID NO: 77)
656	RCTRTCHGCNAGCTNGCYTT!	GGPII-12	(SEQ ID NO: 78)
659	ACHAGAGATGGCTGAG!	GGPI-13	(SEQ ID NO: 79)
660	ACHAGAGATGGCTGAG!	GGPI-13	(SEQ ID NO: 80)
661	CAYCARTNTGGGCHGCA!	GGPII-1	(SEQ ID NO: 81)
662	TTYGTNGTATGAGGCA!	GGPII-4	(SEQ ID NO: 82)
663	AARGCHAYGCNCAYACG!	GGPI-1	(SEQ ID NO: 83)
664	CARGCHAYGCNCAYACG!	GGPI-14	(SEQ ID NO: 84)
665	GTNGCHAYGCNCAYACG!	GGPII-6	(SEQ ID NO: 85)
666	GTNGCHAYGCNCAYACG!	GGPII-6	(SEQ ID NO: 86)
694	NACYTTTTTAAATTTGCG!	GGPI-17	(SEQ ID NO: 87)

FIGURE 20

Degenerate PCR primers

Oligo	Sequence	Peptide	
657	CCGAATTCTGCAGGARAACACACGAYCCGCG!	GGPII-17	(SEQ ID NO: 90)
658	AAGGATCTCTCAGNGTRTANGONCCATNACCATNGG!	GGPII-17	(SEQ ID NO: 91)
667	CCGAATTCTGCAGGCHGAYTCCHGARTAYATG!	GGPII-12	(SEQ ID NO: 92)
668	CCGAATTCTGCAGGCHGAYATYCHGARTAYAT!	GGPII-12	(SEQ ID NO: 93)
669	AAGGATCTCTCAGNCHCATRTAYTCHCCHGARTC!	GGPII-12	(SEQ ID NO: 94)
670	AAGGATCTCTCAGNCHCATRTAYTCHCCTRTCTC!	GGPII-12	(SEQ ID NO: 95)
671	CCGAATTCTGCAGCAYCAROTNTCCGCHGCHAA!	GGPII-1	(SEQ ID NO: 96)
672	CCGAATTCTGCAGATHTTYYTYYATGCAACCHGARG!	GGPII-2	(SEQ ID NO: 97)
673	CCGAATTCTGCAGGCGCHGCHGCHGCHTTCCHGT!	GGPII-3	(SEQ ID NO: 98)
674	CCGAATTCTGCAGTGGTTCGTHGTYATGCAAGG!	GGPII-4	(SEQ ID NO: 99)
677	AAGGATCTCTCAGYTTNGCHGCHCAACCTCTCTG!	GGPII-1	(SEQ ID NO: 100)
678	AAGGATCTCTCAGGCTTCCHGCTTCAATRAAA!	GGPII-2	(SEQ ID NO: 101)
679	AAGGATCTCTCAGACHGGRANGCHGCHGCHGCHG!	GGPII-3	(SEQ ID NO: 102)
680	AAGGATCTCTCAGYTTNGCTTCATNACNACRAAC!	GGPII-4	(SEQ ID NO: 103)
681	CATRTAYTCTRTAYTCTCHGCAAGGATCTCTGCAG!	GGPII-2	(SEQ ID NO: 104)
682	CCGAATTCTGCAGAAAGGNGAYGCHAYACHGAI!	GGPII-1	(SEQ ID NO: 105)
683	CGHGCYAAAGCYTCYTTNGCAAGGATCTCTGCAG!	GGPII-14	(SEQ ID NO: 106)
684	CGHCHAGHGCYTCYTTNGCAAGGATCTCTGCAG!	GGPII-14	(SEQ ID NO: 107)
685	TCHGCAARTANCHGCHAGGATCTCTGCAG!	GGPII-1	(SEQ ID NO: 108)

Unique PCR primers for Factor II

Oligo	Sequence	Comment	
711	CATCGATCTGCAGGCTGATCTCGAGAATATATGTGCA!	3' RACE	(SEQ ID NO: 109)
712	AAGGATCTCTCAGCCCATCTCGAGTCGACATCGATT!	3' RACE	(SEQ ID NO: 110)
713	CCGAATTCTGCAGTGAATCAGCAACTACGAAATGACA!	3' RACE	(SEQ ID NO: 111)
721	CATCGATCTGCAGGCTGATCTCGAGAATATATGTGCA!	5' RACE	(SEQ ID NO: 112)
722	AAGGATCTCTCAGTGAATCTCGAGAATATATGTGCA!	5' RACE; ANCHORED	(SEQ ID NO: 113)
723	AAGGATCTCTCAGGCAAGCACTGAGCACTCTCTTA!	EXON A	(SEQ ID NO: 114)
726	CCGAATTCTGCAGCAAGCACTGAGCACTCTCTTA!	EXON A	(SEQ ID NO: 115)
771	CATCCCCGATGAAAGTCAGAGTCTGTGCGA!	EXONS 3+4	(SEQ ID NO: 116)
772	ATACCCCGGCTGCAGACAAATGAGATTTCACACCTGCG!	EXONS 3+4	(SEQ ID NO: 117)
773	AAGGATCTCTCAGTTTGCAGCTGCAACAGACTCTT!	ANCHORED	(SEQ ID NO: 118)
776	ATACCCCGGCTGCAGATGAGATTTCACACCTGCGTGA!	EXONS 3+4	(SEQ ID NO: 119)

Summary of contiguous GGF-II cDNA structures and sequences

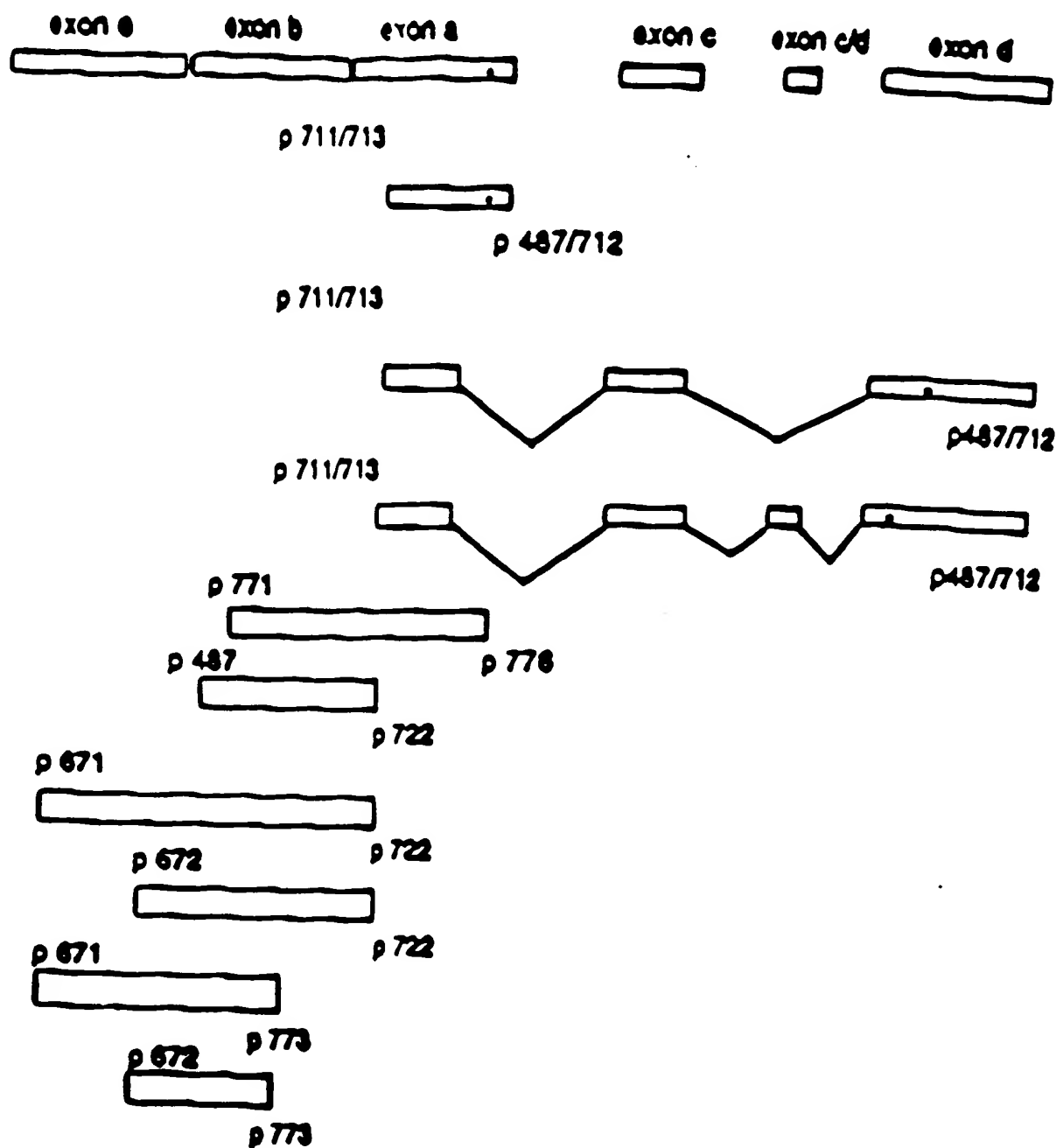


FIGURE 23



FIGURE 24

Alternative gene products of putative bovine GGF-9

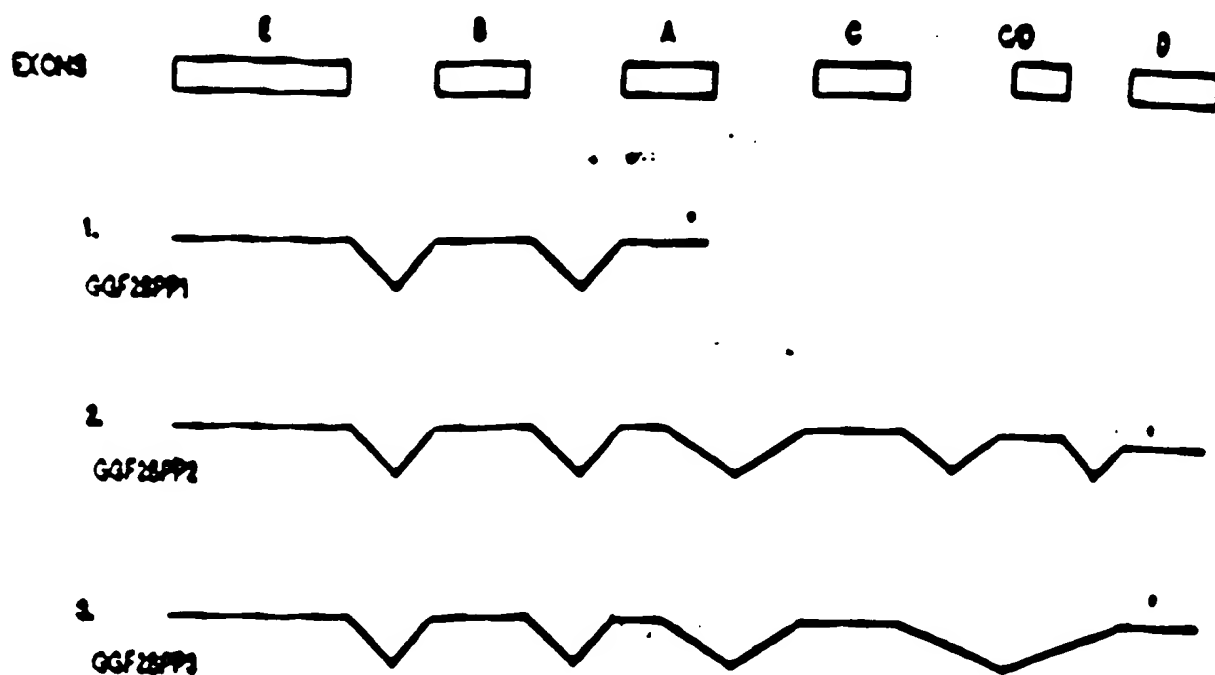


FIGURE 25

007-11 protein identified in deduced sequences of putative 007-11 proteins

Peptide	Pos.	Sequence Match	
II-1	1:	VHQVWAAR HQVWAAR AAGLR	(SEQ ID NO: 120)
II-10	14:	DLLLV GGLR dellev RLGAR	(SEQ ID NO: 121)
II-03	21:	LGAWGPPAFFVYR LLVR lgavghpafpafv RLRD	(SEQ ID NO: 122) (SEQ ID NO: 123)
II-02	41:	YIFTHPELXSSG KEDSR YIFTHPELXSSG GPRRL	(SEQ ID NO: 124) (SEQ ID NO: 125)
II-6	103:	LVLK VAGSR LVLK CETSS	(SEQ ID NO: 126)
I-18	112:	EYKCLKFKWTFQATVH CETSS eysslkfkvflngsel SRDNR	(SEQ ID NO: 127) (SEQ ID NO: 128)
II-12	151:	KSLADSGEYHCK ELRIS KSLADSGEYHCK VTSKL	(SEQ ID NO: 129) (SEQ ID NO: 130)
I-07	152:	ASLADSEYHCK LRISK asladsgeyck VTSKL	(SEQ ID NO: 131) (SEQ ID NO: 132)

FIGURE 26

(SEQ ID NO: 135)

FIGURE 27 3/3

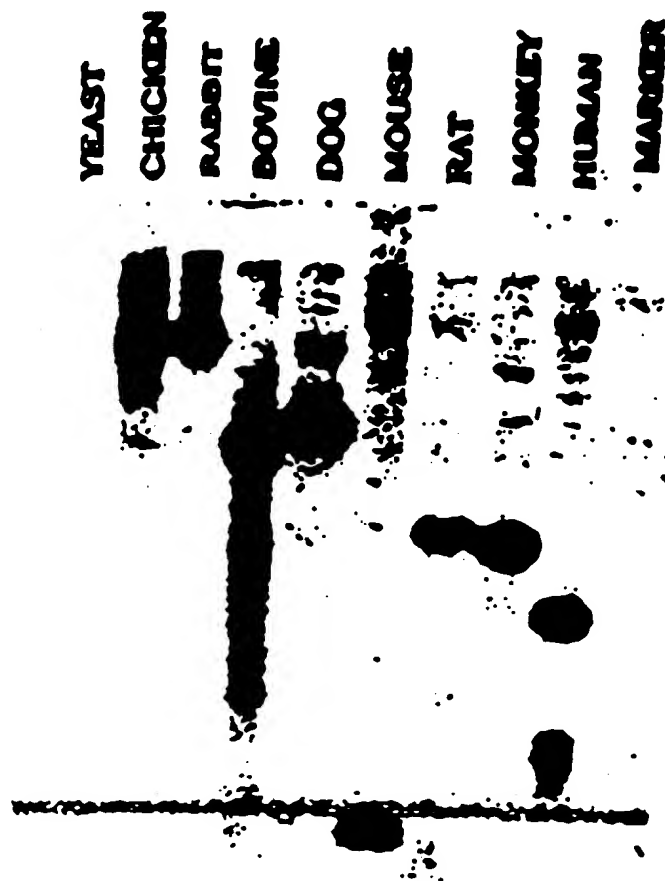
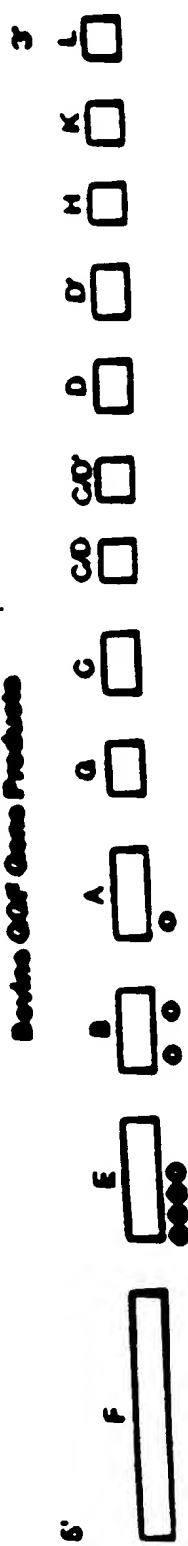


FIGURE 28

FIGURE 29

Decline QOF Game Products



Hexageline



10

3

COOLING SEGMENT P1: (SEQ ID NO: 136)

[illegible]

CODING SECRET 2: (SEQ ID NO: 137)

CCCATCAGTGTGCGCGCGGAAAGCCGCGCGCTTGAAGAAIGGACTGCGCTGCTCAACGCTG 60
 H Q V W A A K A G G L K K D S L L T V R
 GCGTGGCGGCTGTGCGCCACCCCGCCTTCGCCCTCTGCGCGCGCCTCAAGGAGGACAGCA 120
 L G A W G H P A P P S C G R L K E D S R
 GGTACATCTTCTTCAATGGAAGCCGAGGCCAACAGCAAGCGGCGCGCGCGCGCTTCCGA 180
 Y I P P H E P E A N S S G G P G R L P S
 GCCTGCTTCCCGCTCTCGAGACGGGCGCGAACCTCAAGAGGAGGTCAGCCCGGCTGCTG 240
 L L P P S R D G P E P Q E G G Q P G A V
 TCCAAAGCTGCG 300

CODING SEGMENT B: (SEQ ID NO: 138)

L P P R L K E N E S Q E S V A G S R L V
 CCTTCCCTCCCCCTTGAAGAGATGAAGAGTCAGGAGTCTGTGCCAGGTTCCAACTAG 60
 |||||
 ccttgcctccccgattgaaagagatgaaagccagggaatcggtgcagggtccaaactag
 Q A
 L R C E T S S E Y S S L K P E V P E N G
 TCGTTCGGTCCGAGACCAGTTCTGAATACTCCTCTCTCAAGTTCAAGTGGTTCAAGATG 120
 |||||
 tccctcggtgtgaaaccagttctgaatactcctctctcagattcaagtgggtcaaggaatg
 R
 S E L S R K N K P Q N I K I Q E R P G
 GGAGTGAATTAAGCCGAAAGAACAAACCAAAACATCAAGATACAGAAAGCCCGGG 170
 |||||
 ggaatgaattgaatcgaataaacacacacaaatatcaagatacaaaagccagg
 H H K

CODING SEGMENT A: (SEQ ID NO: 139)

K S E L R I S K A S L A D S G E Y N C K
 GAAGTCAGAACTTCCATTAGCAAGCGTCACTGCGCTGATTCTCGAGATATATGTGCAA 60
 |||||
 gaagtcaaggacttcgcattaacaaagcatcactgggtgattctggagagtatatgtgcaa
 H
 V I S K L G N D S A S A N I I V E S N
 AGTGATCAGCAAACTAGCAAAATGACAGTGCCTCTGCCAACATCACCATTGTGAGTCAA 120
 |||||
 agtgatcagcaaaattaggaaatgacagtgcctctgccaaatcaccatcgtggaatcaa
 A
 CG 122
 ||
 CG

CODING SEGMENT A': (SEQ ID NO: 140)

TCTAAAACTACAGAGACTGTATTTTATGATCATCATAGTTCTGTCAATATACTTAAAC 60
 K S E L R I S K A S L A D
 CGCTTTGCTCCTGATCTTTGTAGCAAGTCAGAACTTCCGATTAGCAAGCGTCACTGCGTG 120
 S G E Y N C K V I S K L G N D S A S A N
 ATTCTCGAGAAATATATGTGCAAGTATCAGCAAACTAGCAAAATGACAGTGCCTCTGCCA 180
 I T I V E S N G K R C L L R A I S Q S L
 ACATCACCATTGTGAGTCAAGCGTAAGAGATGCCTACTGCGTCTATTCTCAGTCTC 240
 R G . . . K . . . C . . .
 TAAAGGATTCATCAAGGATATGTCTCTACACTTCAATCAGCGAGGTTGTGTAAATGTCA 300

360
417

(SEQ ID NO: 141)

60

102

(SDQ ID NO: 160)

60

120

120

FIGURE 30 4/8

CODING SEGMENT C/D: (SEQ ID NO: 142)

K C Q P G F T G A R C T E N V P N E V Q
 AAGTGCCCAACCTGGATTCACTGGAGCGAGATGTACTGAGAATGTGCCCATCAAAGTCCAA 60
 |||||
 aagtgcccaacctggattcactggagcgaagatgtactgagaatgtgcccataaaagtccaa

T Q E
 ACCCAAGAA 69
 |||||
 aaccaagaa
 N

CODING SEGMENT C/D': (SEQ ID NO: 143)

K C P N E F T G D R C Q N Y V N A S F Y
 AAGTGCCCAAAATGAGTTTACTGGTATCGCTGCCAAAAGTACGTAATGCCAGCTTCTAG 60
 |||||
 aagtgcccaaatgagtttactggatcgctgccaaaagtacgtaaatggcagcttctag

CODING SEGMENT D: (SEQ ID NO: 144)

S T S T P P L S L P E Q
 AGTACGTCCCACTCCCTTTCTGTCTCTGCTGAATAG 36
 |||||
 agtacgtccactccctttctgtctctgctgaatag

CODING SEGMENT D': (SEQ ID NO: 145)

K E L G I E F N E
 aagcatcttgggattgaatttatggag 27

ACATAAGCTTATAGCTGAGCTAAGGAGAAACAGGCTCCACAGATCCAAAGCATGCAAG?
N N L I A E L R R N K A N R S R C N Q I
CCAGCTTTCGGCAACTCATCTTAGAGCTTCTTCCATTCCCCATTGGGCTTCATTCTGTAA
Q L S A T E L R A S S I P E W A S F S E
GACCCCTTGGGCTTCAAGCAAG
T P N P L G R

CODING SEGMENT L: (SEQ ID NO: 147)

Y V S A N T T P A R N S P V D F E T P S
GTATGTATCAGCAATGACCAACCCCTGCTGATGTACCTGTAGATTTCACACGCCAAG 60
|||||
gtatgtgtcagccatgaccaccccggctcgtatgtcacctgtagatttcacacagccaag

S P K S P P S E N S P P V S S T T V S N
CTCCCCCAAGTCACCCCTTCGGAAATGTCCCCGCCCCGTGTCCAGCAAGACGGTCTCCAG 120
|||||
ctcccccaaatcggcccccttcggaaatgtctccaccctgtgtccagcatgacgggtgtccat

P S N A V S P F V E E E R P L L L V T P
GCCCCCTCATGGCGGTCAAGTCCCTTGTGGAAGAGAGAGACCCCTGCTCCTTGTGACGCC 180
|||||
gccttccatggcggtcagcccccttcattggaagaaagagagacctctacttctcgtgacac

P R L R E K - Y D E E A Q Q F N S P E C
ACCACTGCTCGGGAGAAAG...TATGACCAACCAAGCCACCAATTCAACTCGTTCCACTG 240
|||||
accaaggtcgcgggagaaagagtttgaccatcacctcagcagttcagctccttccacaa

H P A E S N S L P P S P L R I V E D S
CAACCCCGCCATGACAGCAACAGCCTGCCCCCAGCCCCCTGAGGATAGTGGAGGATGA 300
|||||
caaccccgagcatgacagtaaacagcctccctgctagcccccttgaggatagtggaggatga

E Y E T T Q E Y E P A Q E P V K E L T N
CGAATATGAAACGACCCAGGAGTACCAACCAAGCTCAAGAGCCCGTTAAGAAACTACCTA 360
|||||
ggagtatgaaacgacccaagagtagagccagcccaagagcctgttaagaaactcgcac

S S R R A K R T K P N G N I A N R L E N
CAGCAGCCGGCGGGCCAAAAGAACCAAGCCCCAATGGTCACATTGCCACAGGTTGGAAAT 420
|||||
...tagccggcgggccaaaagaaaccaagccccaatggccacattgctaacagattggaaat

[illegible]

100

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c.

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E

11

3. 2.

GGP28PP2 nucleotide sequence and deduced protein sequence

CATCATGTGTGGGCGGGGAAAGCGGGGGCTTGAAGAAAGTCTGGCTGCTACCGTTCG 10
 H Q V W A A K A G G L K K D S L L T V R
 CTGGCGCGCTGGGCGCCACCCCGCTTCCCTCTCTGCGGGGGCTCAAGGAGGACAGCAGG 120
 L G A W G H P A P P S C G R L K E D S R
 TACATCTTCTTCATGGAGCGCCAGCGCCAAAGCAAGCGGGCGGCGCGCGCGCGCTCCAGC 180
 Y I P P H E P E A H S S G G P G R L P S
 CTCTCTCCCTCTCTCTAGAGCGGGCGGAACTCAAGAAAGAGTCAAGCCCGGTGCTGTG 240
 L L P P S R D G P S P Q S G G Q P G A V
 CAAGGTGCGCTTGGCTTCCCTCGCTTCAAGAGATGAAGAGTCAAGAGTCTGTGGCAGGT 300
 Q R C A L P P R L K S H K S Q E S V A G
 TCCAACTAGTGCTTCCGTGCGAGACCAAGTTCTCAATAGTCTCTCTCAAGTTCAAGTGG 360
 S K L V L R C E T S S E Y S S L K P K H
 CTCAGAAATCGGAGTGAATTAAAGCCGAAAGCAAAAGCAAAATCAAGATACAGAA 420
 P K H G S E L S R K H K P E H I K I Q K
 AGGCGCGCGGAAAGTCAAGAACTTCCATTAGCAAGCGTCACTGGCTGATTCTCGAGAAATAT 480
 R P G K S E L R I S K A S L A D S G E Y
 ATGTGCAAAAGTGATCAGCAAACTAGCAAAATGAAGTGGCTCTGCGCAATCAACCATTTGTG 540
 H C K V I S K L G H D S A S A H I T I V
 GAGTCAAGCGCCACATCCACATCTACAGCTGGGACAAAGCATCTTGTCAAGTGTGCAAG 600
 E S H A T S T S T A G T S H L V K C A E
 AAGGAGAAAAGCTTCTGTGTGAATCGAGCGGAGTCTTCAATGGTCAAGAGCTTTCAAA 660
 K E K T P C V H G G E C P H V K D L S H
 CCTTCAAGATACTTGTGCAAGTGGCAAGCTCGATTCACTGAGCGGAGATGTACTGAGAA 720
 P S R Y L C K C Q P G P T G A R C T E H
 GTGCCCATGAAGTCCAAAGCCCAAGAAAGTGGCCAAATGAAGTTTACTGGTCAATCGCTGC 780
 V P H E V Q T Q E K C P H E P T G D R C
 CAAAAGTACGTAATGGCCAGCTTCTACAGTACGTCCACTCCCTTTCTGTCTCTGCTGAA 840
 Q H Y V H A S P Y S T S T P P L S L P E
 TAGCGCATCTCAGTGGTGGCGCTTCTTGTGCGGCAATCTCCCTCAGATTCTCTCCAG 900
 .
 AGCTAGATGCGTTTTTACCAGGTCTAACATGACTGCGCTGTGCTGTGCGCATGAGAACATT 960
 AACACAAGCGATTGTATGACTTCCCTGTGTCGTGACTAGTGGGCTCTGAGCTACTCGTAG 1020
 GTGCGTAAGGCTCCAGTGTTTCTCAATTGATCTCAATTACTGTGATGCCACATGATAG 1080
 TCCCTCTCAAGCGAGTGCAATGACAAATAAAGCGCTTCAAAAGTCAAAAAAAAAA 1140

FIGURE 31 2/2

TGA CTTCCTCTCTCCGTGA CTAGTCCCTCTCTCAGCTACTCGTAGGTCCGTAAAGGCTCCAG 1380
 TGTTCCTGAATTGATCTTGAATTACTGTGATACGACATGATAGTCCCTCTCAGCCAGT 1440
 CAATGACATAAAGGCTTGA AAAAGTCTCACTTTTATTGAGAAAATAAAAATCGTTCCAG 1500
 CCGACAGTCCCTCTTCTTTATAAAAAGACCCTATCCTTGAAAAGGAGGTGTGTTAAGTT 1560
 TAACCAGTACACACTTGAAATGATCGTAA GTTCGGTTCCGTTTCAGAA TGTGTTCTTTCTG 1620
 ACAAATAAA CAGATAAAAAAAAAAAAAA 1680

CGP28994 nucleotide sequence and deduced protein sequence

GAAGTCAGAACTTCCATTAGCAAAGCGTCACTCGGCTCAATTCGAGAAATATGTGCCAA 60
 K S E L R I S K A S L A D S G S Y N C R
 AGTGATCAGCAAAGTACGAAATGACAGTGGCTCTGCCAAATCACCATTGTGAGTCAA 120
 V I S K L G N D S A S A N I T I V E S N
 CGCCACATCCACATCTACAGCTGGGACAAAGCCATCTTGTCAAGTGTGCAGAGAGAGAA 180
 A T S T S T A G T S E L V K C A E K E E
 AACTTTCTGTGTGAATGGAGCGGACTGCTTCATGGTGAAGAAGCTTTCAAATCCCTCAAG 240
 T P C V N G G D C F N V K D L S N P S R
 ATACTTGTCAAAGTCCCAAGCTCGATTCACTCGAGCCAGATGTACTGAGAAATGTGCCCA 300
 Y L C K C Q P G F T G A R C T E N V P N
 GAAAGTCCAAACCCAAAGAAAGCCGAGGAGCTGTACCAAGAGAGTGTCTACCAATTAC 360
 K V Q T Q E K A E E L Y Q K R V L T I T
 CGGCATTTCATCGCGCTGCTGTGGTTGGCATCATGTGTGTGCTGTCTACTGCAAAAC 420
 G I C I A L L V V G I N C V V V Y C K T
 CAAGAAACAAACGAAAGAAAGCTTCATGACCGGCTTCGGCAGAGCTTCGGTCTGAAGAAA 480
 K K Q R K K L E D R L R Q S L R S E R N
 CACCATCATGAACGTAGCCAAAGGCCCCAACCACCCCAATCCGCCCCCGAGAACGTGCA 540
 T N N N V A N G P E E P N P P P E N V Q
 GCTGGTGAATCAATACGTATCTAAAAATGTTCATCTCTAGCGAGCATATTGTTCAGAGAGA 600
 L V N Q Y V S K N V I S S E E I V E R E
 GCGCGAGAGCTCTTTTCCACAGTCACTACACTTCGACAGCTCATATTCCACTACTGT 660
 A E S S P S T S E Y T S T A E E S T T V
 CACTCAGACTCCCACTCAAGCTGGAGCAATGGACACACTCAAGCATATTTCGGAAG 720
 T Q T P S E S N S N G E T E S I I S E S
 CCACTCTGTCAATCGTATGTCAATCGTAGAAAACAGTAGGCAAGCAAGCCCACTGGGG 780
 H S V I V E S S V E N S R E S S P T G G
 CCGCAGAGGAGCTCTCAATGGCTTGGGAGGCGCTCTGTAATGTAAAGCTTCTCAGGCA 840
 P R G R L N G L G G P R E C H S P L R E
 TCCAGAGAAACCCCTGACTCTTACCGAGACTCTCTCTCATAGTCAAAGACATAACCTTAT 900
 A R E T P D S Y R D S P E S E R E N L I
 AGCTGAGCTAAGGAGAAACAAAGGCCACAGATCCAAATGATGCAGATCCAGCTTTCCGC 960
 A E L R R N K A E R S K C N Q I Q L S A
 AACTCATCTTAGAGCTTCTTCCATTCCCCATTGGGCTTCATTCTCTAAGACCCCTTGGCC 1020
 T H L R A S S I P N W A S P S K T P W P
 TTEAGGAAGGTATGTATCAGCAATGACCACCCCGGCTCGTATGTACCTGTAGATTTCCA 1080
 L G R Y V S A H T T P A R N S P V D F H
 CAGCCCAAGCTCCGCAAGTCAAGCCCTTCGCAATGTCTTGGCCCTGTCCAGCACGAC 1140
 T P S S P Y S P P S E M S P P Y S S T T

FIGURE 33 2/2

GGTCTCCATGCCCTCCATGCGCGTCACTCCCTTCGTGGAAGAGGAGAGACCCCTGCTCT 1200
 V S N P S N A V S P P V E E E R P L L L
 TGTACGCCAACCACCGCTGCGCGAGACTATGACCAACAAGCCCAAGCAATTCAGTCTT 1260
 V T P P R L R E K Y D N N A Q Q P N S P
 CCACTGCAACCCCTGCGCATGAGAGCAACAGCTGCCCCCAGCCCCCTGAGGATAGTGA 1320
 H C N P A E E S N S L P P S P L R I V E
 GGATACGGAATATGAAACGACCCAGGAGTACGAACCAAGTCAAGAGCCCGTTAAGAACT 1380
 D E E Y E T T Q E Y E P A Q E P V K E L
 CACCAACAGCAGCCCGCGCGCAAGCAACCAAGCCCAATGGTCAATTCGCCACAGCTT 1440
 T N S S R R A K E T K P N G N I A E R L
 GGAATCGACAAACAACAGCGCGTACAGCAGTAACTCAGAGAGCGAAACAGGATGA 1500
 E N D N N T G A D S S N S E S E T E D E
 AAGAGTAGGAGAAGATACGCTTCTGCGGCATACAGAAACCCCTGCGACCCAGTCTCGA 1560
 R V G E D T P P L A I Q N P L A A S L E
 GCGCGCCCTGCGCTTCCGCTGCGTCAAGCAGGACTAAACCAACAGCGCGCTTCTCTCC 1620
 A A P A P R L V D S R T N P T G G P S P
 GCAGGAAGAATTGCAGGCCAGGCTCTCCGTGTAAATCGCTAACCAAGACCCCTATCGCTGT 1680
 Q E E L Q A R L S G V I A N Q D P I A V
 CTAAACCGAAATACACCCATAGATTCACTGTAAACTTTATTTTATATAATAAAGTAT 1740
 TCCACCTTAATTAAACAAAA 1764

FIGURE 34

.
GGF2D0005KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYVMASFY 1
GGF2D0004KCAEKEKTFCVNGGDCFMVKDLSNPSRYLCKCQPGFTGARCTENVPWKVQ 2
DEGE ECLRKYKDFCIH - GECKYVKELRAPS — CKCQQEYFGERCGEKSARKHS 3

1(SDQ ID NO: 151)

2(SDQ ID NO: 152)

3(SDQ ID NO: 153)

FIGURE 35

200 kDa tyrosine phosphorylation compared with mitogenic activity

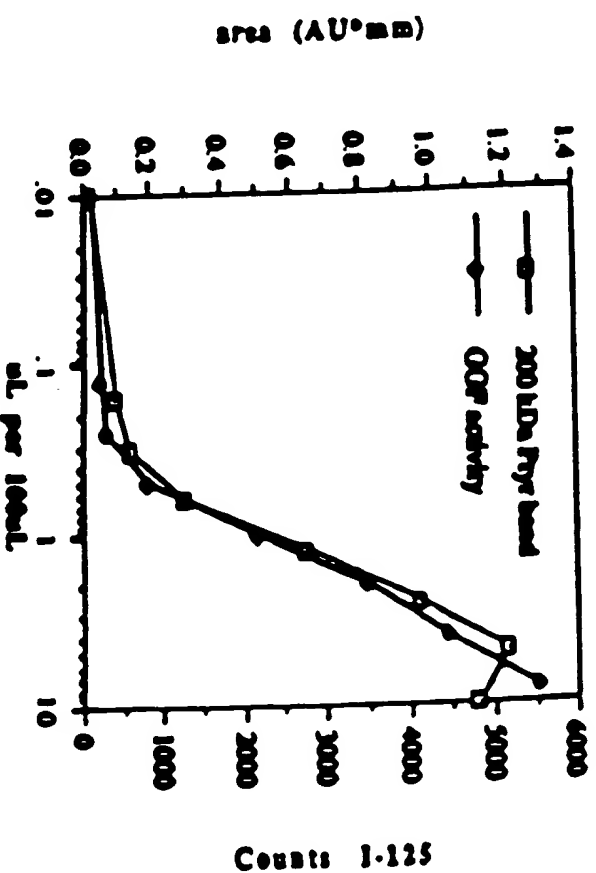


FIGURE 36 172

GGT/REGULON SPLICING VARIANTS

F-B-A'

F-B-A-C-C/D-D
F-B-A-C-C/D-E
F-B-A-C-C/D-E-L
F-B-A-C-C/D-E-K-L
F-B-A-C-C/D-D'-E
F-B-A-C-C/D-D'-E-L
F-B-A-C-C/D-D'-E-K-L
F-B-A-C-C/D'-D
F-B-A-C-C/D'-E
F-B-A-C-C/D'-E-L
F-B-A-C-C/D'-E-K-L
F-B-A-C-C/D'-D'-E
F-B-A-C-C/D'-D'-E-L
F-B-A-C-C/D'-D'-E-K-L
F-B-A-C-C/D'-D
F-B-A-C-C/D'-D-E
F-B-A-C-C/D'-D-E-L
F-B-A-C-C/D'-D-E-K-L
F-B-A-C-C/D'-D'-E
F-B-A-C-C/D'-D'-E-L
F-B-A-C-C/D'-D'-E-K-L

F-E-B-A'

F-E-B-A-C-C/D-D
F-E-B-A-C-C/D-E
F-E-B-A-C-C/D-E-L
F-E-B-A-C-C/D-E-K-L
F-E-B-A-C-C/D-D'-E
F-E-B-A-C-C/D-D'-E-L
F-E-B-A-C-C/D-D'-E-K-L
F-E-B-A-C-C/D'-D
F-E-B-A-C-C/D'-E
F-E-B-A-C-C/D'-E-L
F-E-B-A-C-C/D'-E-K-L
F-E-B-A-C-C/D'-D'-E
F-E-B-A-C-C/D'-D'-E-L
F-E-B-A-C-C/D'-D'-E-K-L
F-E-B-A-C-C/D'-D
F-E-B-A-C-C/D'-D-E
F-E-B-A-C-C/D'-D-E-L
F-E-B-A-C-C/D'-D-E-K-L
F-E-B-A-C-C/D'-D'-E
F-E-B-A-C-C/D'-D'-E-L
F-E-B-A-C-C/D'-D'-E-K-L

F-B-A-G-C-C/D-D
F-B-A-G-C-C/D-E
F-B-A-G-C-C/D-E-L
F-B-A-G-C-C/D-E-K-L
F-B-A-G-C-C/D-D'-E
F-B-A-G-C-C/D-D'-E-L
F-B-A-G-C-C/D-D'-E-K-L
F-B-A-G-C-C/D'-D
F-B-A-G-C-C/D'-E
F-B-A-G-C-C/D'-E-L
F-B-A-G-C-C/D'-E-K-L
F-B-A-G-C-C/D'-D'-E
F-B-A-G-C-C/D'-D'-E-L
F-B-A-G-C-C/D'-D'-E-K-L
F-B-A-G-C-C/D'-D
F-B-A-G-C-C/D'-D-E
F-B-A-G-C-C/D'-D-E-L
F-B-A-G-C-C/D'-D-E-K-L
F-B-A-G-C-C/D'-D'-E
F-B-A-G-C-C/D'-D'-E-L
F-B-A-G-C-C/D'-D'-E-K-L

F-E-B-A-G-C-C/D-D
F-E-B-A-G-C-C/D-E
F-E-B-A-G-C-C/D-E-L
F-E-B-A-G-C-C/D-E-K-L
F-E-B-A-G-C-C/D-D'-E
F-E-B-A-G-C-C/D-D'-E-L
F-E-B-A-G-C-C/D-D'-E-K-L
F-E-B-A-G-C-C/D'-D
F-E-B-A-G-C-C/D'-E
F-E-B-A-G-C-C/D'-E-L
F-E-B-A-G-C-C/D'-E-K-L
F-E-B-A-G-C-C/D'-D'-E
F-E-B-A-G-C-C/D'-D'-E-L
F-E-B-A-G-C-C/D'-D'-E-K-L
F-E-B-A-G-C-C/D'-D
F-E-B-A-G-C-C/D'-D-E
F-E-B-A-G-C-C/D'-D-E-L
F-E-B-A-G-C-C/D'-D-E-K-L
F-E-B-A-G-C-C/D'-D'-E
F-E-B-A-G-C-C/D'-D'-E-L
F-E-B-A-G-C-C/D'-D'-E-K-L

FIGURE 36

007/REDBOULIN IMPLICITING VARIANTS CONTINUED

E-B-A'

E-B-A-C-C/D-D
E-B-A-C-C/D-E
E-B-A-C-C/D-E-L
E-B-A-C-C/D-E-K-L
E-B-A-C-C/D-D'-E
E-B-A-C-C/D-D'-E-L
E-B-A-C-C/D-D'-K-K-L
E-B-A-C-C/D'-D
E-B-A-C-C/D'-E
E-B-A-C-C/D'-E-L
E-B-A-C-C/D'-E-K-L
E-B-A-C-C/D'-D'-E
E-B-A-C-C/D'-D'-E-L
E-B-A-C-C/D'-D'-E-K-L
E-B-A-C-C/D-C/D'-D
E-B-A-C-C/D-C/D'-E
E-B-A-C-C/D-C/D'-E-L
E-B-A-C-C/D-C/D'-E-K-L
E-B-A-C-C/D-C/D'-D'-E
E-B-A-C-C/D-C/D'-D'-E-L
E-B-A-C-C/D-C/D'-D'-E-K-L

E-B-A-C-C-C/D-D
E-B-A-C-C-C/D-E
E-B-A-C-C-C/D-E-L
E-B-A-C-C-C/D-E-K-L
E-B-A-C-C-C/D-D'-E
E-B-A-C-C-C/D-D'-E-L
E-B-A-C-C-C/D-D'-E-K-L
E-B-A-C-C-C/D'-D
E-B-A-C-C-C/D'-E
E-B-A-C-C-C/D'-E-L
E-B-A-C-C-C/D'-E-K-L
E-B-A-C-C-C/D'-D'-E
E-B-A-C-C-C/D'-D'-E-L
E-B-A-C-C-C/D'-D'-E-K-L
E-B-A-C-C-C/D-C/D'-D
E-B-A-C-C-C/D-C/D'-E
E-B-A-C-C-C/D-C/D'-E-L
E-B-A-C-C-C/D-C/D'-E-K-L
E-B-A-C-C-C/D-C/D'-D'-E
E-B-A-C-C-C/D-C/D'-D'-E-L
E-B-A-C-C-C/D-C/D'-D'-E-K-L

AGCCATCTTGTCAAGTGTGCAGAGAACGAGAAAACCTTTCTGTGTGAATGGAGGCGAGTCC
S H L V R C A E R E R T P C V N G G E C
TTCATGCTGAAAGACCTTTCAAATCCCTCAAGATACTTGTGCAAGTGCCCAAATGAGTTT
P N V K D L S N P S R Y L C R C P N E P
ACTGGTGATCGCTGCCAAAAGTACGTAATGGCCAGCTTGTACAGTACGTCCACTCCCTTT
T G D R C Q N Y V N A S P Y S T S T P P
CTGTCTCTGCCTGAATAG
L S L P E *

(SEQ ID NO: 154)

FIGURE 37

EGFL2

AGCCATCTTGTCAGTGTGCAGAGACGAGAAAACCTTCTGTGTGAATGGAGCCGAGTGC
S N L V K C A E E E K T F C V N G G E C
TTCATGCTGAAAGACCTTTCAAATCCCTCAAGATACTTGTGCAAGTCCCACTGGATTG
F N V K D L S N P S R Y L C K C Q P G F
ACTCGAGCGAGATGTACTGAGAAATGTGCCCATGAAAGTCCAAACCCAGAAAAGCCGAG
T G A R C T E N V P N K V Q T Q E K A E
GAGCTCTACTAA
E L Y •

(SEQ ID NO: 155)

FIGURE 38

ACCCATCTTGTCAAGTGTGCAGAGAGGAGAAAAGTTTCTGTGTGAATGGAGGGGAGTGC
 S H L V R C A E K E K T P C V N G G E C
 TTCATCGTGAAAGACCTTTCAATCCCTCAAGATACTTGTGCAAGTGGCCAAATGAGTTT
 P H V K D L S N P S R Y L C K C P H E P
 ACTCGTGATCGGTGCCAAAAGTACCTAATGGCCAGCTTCTACAAAGCGGAGGAGCTCTAC
 T G D R C Q N Y V H A S P Y K A E E L Y
 TAA
 .

(SEQ ID NO: 156)

FIGURE 39

IGFLA

AGCCATCTTGTCAAGTGTGCAGAGAGGACAAAACCTTCTGTGTGAATGGAGCGGAGTGC
S H L V K C A E E E K T P C V N G G E C
TTCATCGTGAAAGACCTTTCAATCCCTCAAGATACTTGTCAGTGCCCAAATGAGTTT
P H V K D L S N P S R Y L C K C P N E P
ACTGGTGATCGCTGCCAAAACCTAGCTAATCGCCAGCTTCTACAAGCATCTTGGGATTGAA
T G D R C Q N Y V N A S P Y K E L G I E
TTTATCGAGAAAGCGGAGGAGCTCTACTAA
P H E K A E E L Y •

(SEQ ID NO: 157)

FIGURE 40

EGFLS

AGCCATCTTGTCAAGTGTGCAGACAGGAGAAAACCTTCTGTGTGAATGGAGGCGAGTGC
S N L V K C A E K E K T P C V N G G S C
TTCATGGTGAAAGACCTTTCAAATCCCTCAAGATACTTGTGCAAGTGCCTCACTGGATTG
P N V K D L S N P S R Y L C K C Q P Q P
ACTGGAGCGAGATGTACTGAGAATGTGCCCATGAAAGTCCAAACCCAAAGAAAAGTGCCTCA
T G A R C T E N V P N K V Q T Q E K C P
AATGAGTTTACTGGTGATCGCTGCCAAAACCTACGTAATGCCAGCTTCTACAGTACGTC
N E P T G D R C Q N Y V N A S P Y S T S
ACTCCCTTTCTGTCTCTGCCTCAATAG
T P P L S L P E .

(SEQ ID NO: 158)

FIGURE 41

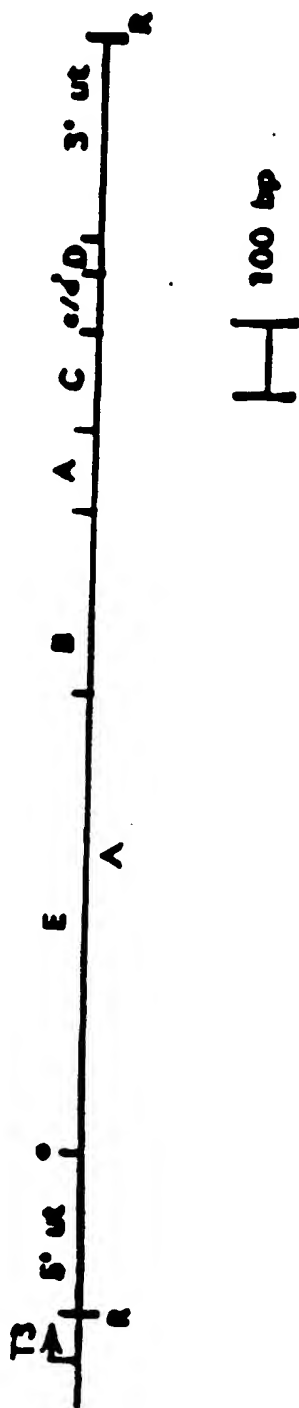
AGCCATCTTGTCTAAGTGTGCAGAGACGGAGAAAACCTTTCTGTGTGAATCGAGCGGAGTCC
 S N L V K C A E K E K T P C V H G G E C
 TTCATGGTGAAAGACCTTTCAATCCCTCAAGATACTTGTGCAAGTGGCAACCTGGATTG
 P H V K D L S N P S R Y L C K C Q P G P
 ACTCGAGCGAGATGTACTGAGAAATGTGCCCATGAAGTCCAAACCCAGAAAAGTGGCCCA
 T G A R C T E N V P H K V Q T Q E K C P
 AATGAGTTTACTGGTGATCGCTGCCAAAACCTACGTAATGCCAGCTTCTACAAAGCGGAG
 N E P T G D R C Q H Y V N A S P Y K A E
 GAGCTCTACTAA
 E L Y •

(SEQ ID NO: 159)

FIGURE 42

GGF2HBS5

FIGURE 43



[illegible]

FIGURE 44 *i/3*

[illegible]

FIGURE 45A

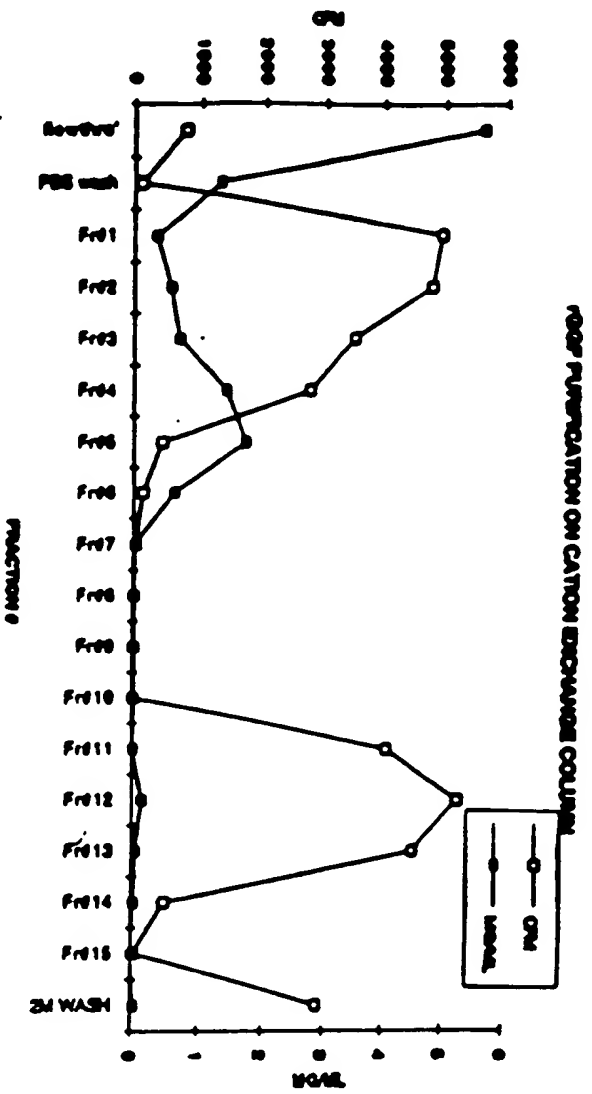
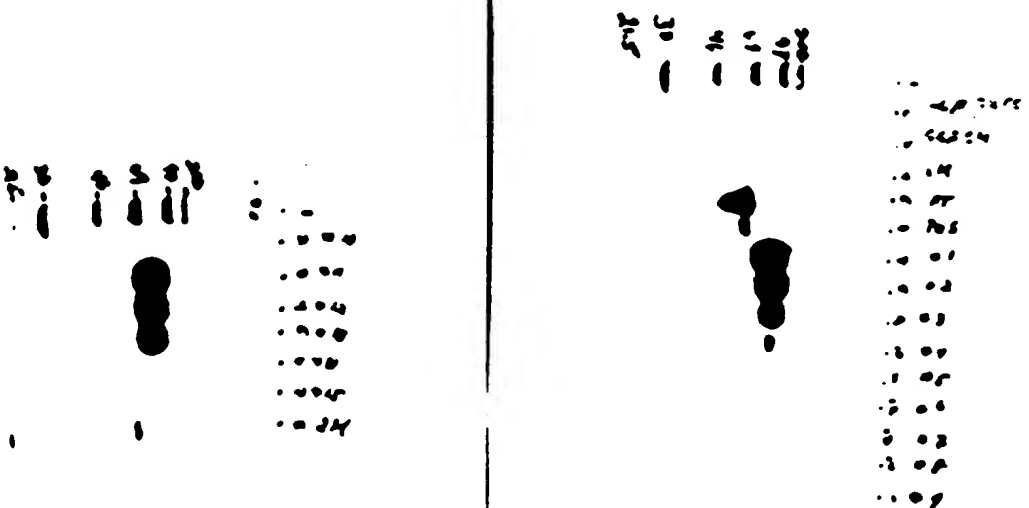


FIGURE 45B



2

**INTERSTATE COMMERCE COMMISSION
WASHINGTON, D.C. 20420**

II-3 II-4

61 VC752778VQSVQELAGNULVYIDRVTNQLNQQAALZSRUAAUUGERANVQGRLEP7AA
•

II-1
II-10

121 OPALPAPAEPLLAUCITYVWUTLAVFVSALSGOBEAFTLVKTVQVVAVLACRJSDEL
II-2

L7VRL0THQWPNPFCOLLEIDRNL77HEZDAWEDROLNLTUASFTTLETGONLJUY

3

COPTD05	361
SEQ ID NO:	171
SEQ ID NO:	172
CODPRS	1

R K Q D VP OP R Y

II-6	II-10	II-14	II-11	I-7, IX-12,
			II-13	

260 LYCENOSTICTUS IN THE GENUS PTILINOPODUS IN THE ATLANTIC
250 OCEAN .
50
50

1
III-12
3

113	INVESTIGATING.....	ASST
113	INVESTIGATING.....	ASST
113	INVESTIGATING.....	ASST

111-15

173 A

1.

413
212
212

FIGURE 46

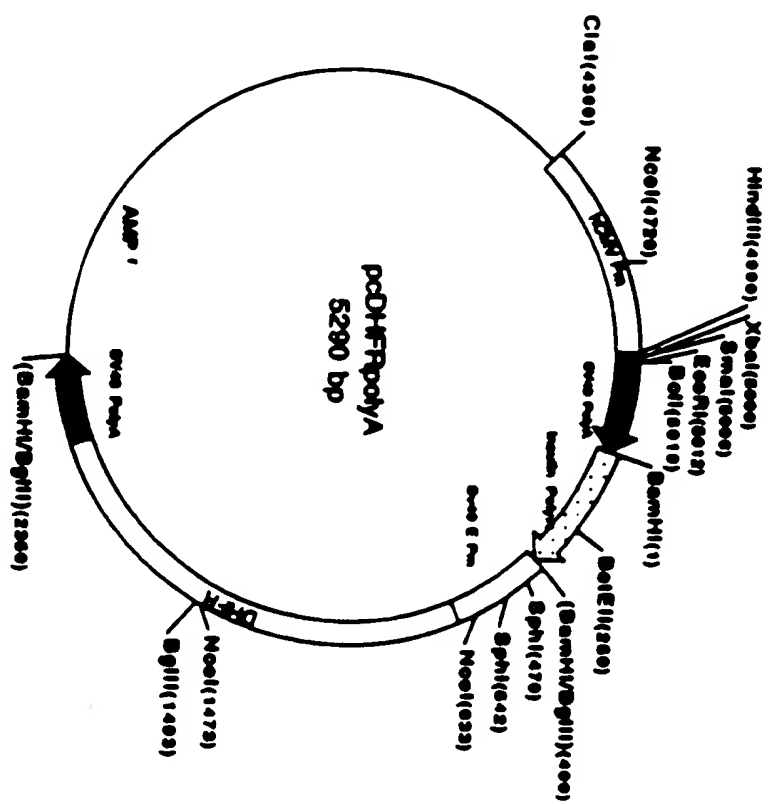


FIGURE 47